

## **REMARKS**

### Introductory Comments

Reconsideration of the above-identified application in view of the foregoing arguments is respectfully requested.

Claims 52-81 are pending. Claims 62-69 and 71-76 remain withdrawn from consideration. Claims 52-61, 70 and 77-81 are under consideration.

### Rejection of Claims 52-61, 70 and 77-81 Under 35 U.S.C. § 101

#### And § 112, First Paragraph

Claims 52-61, 70 and 77-81 are rejected under 35 U.S.C. § 101 and § 112, first paragraph, for the reason contained in the previous Office Action. The Examiner contends that the Declaration of Dr. Granados is germane to the rejection at issue and that it fails to provide any evidence that the BS322 polypeptides according to SEQ ID NOS: 25-28 are equivalent to the NY-BR-1 breast cancer antigen polypeptide. Applicants respectfully traverse this rejection.

As submitted by Applicants in their previous responses, the Dirk Jager et al. article “Identification of Tissue-specific Putative Transcription Factor...” support Applicants’ contention that SEQ ID NOS: 24-28 as claimed are useful as required by 35 U.S.C. § 101 and § 112, first paragraph. The Jager et al. article shows that the gene NY-BR-1 is one of the genes responsible for breast cancer. The gene has 37 exons. See the abstract. Applicants have shown in previous responses in Exhibit A, the 100% alignment match and homology between NY-BR-1 and a nucleotide sequence designated BS322 (SEQ ID NO: 9). Nucleotide sequence BS322 or SEQ ID NO: 9 as described in the instant specification, encodes the polypeptide sequences designated SEQ ID NOS: 24-28. These polypeptides are useful in the detection of breast disease which Examiner has refuted.

The Examiner contends in the previous Office Actions that the alignment match between BS322 and NY-BR-1 does not prove that BS322 is the same molecule as NY-BR-1 since 1143 nucleotides are unaccounted for. The Examiner uses this single basis to support her reason why SEQ ID NOS: 24-28 are not useful in the detection of breast disease. Although Applicants appreciate the Examiner’s detailed analysis, Applicants respectfully traverse the rejection and contend this line of reasoning is flawed for the reason set forth below.

Applicants agree with the Examiner’s observation that the alignment consensus between BS322 and NY-BR-1 does not prove BS322 is the exact same molecule of NY-BR-1. However, the 100% consensus between these two molecules over one thousand nucleotides indicates that BS322 could be a splice variant of NY-BR-1. Applicants have attached herein a portion of a BLAST result for AF269087 (NY-BR-1) versus the human genome. As the Examiner can see, the junctions of the exons for the gaps match those that are in the BS322 molecule. Specifically, three exons that account for gaps are at the positions of 3013-3200, 3197-4116 and 2796-3014. This information clearly provides evidence that BS322 is a splice variant of NY-BR-1.

As indicated in the Jager et al. article, NY-BR-1 comprises 37 exons. Exons, also known as expressed sequences, are defined as a portions of a gene

that appear in both the primary and mature mRNA transcripts (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999). Thus, one of ordinary skill in the art would recognize that although BS322 is not the exact molecule of NY-BR-1, the fact that there is a 100% consensus homology between the two molecules for over 1000 nucleotides of the exons indicates that one is a splice of another and would have significant commonalities. It is well known in the art that introns may be excluded from splices which maintain the functionality of a gene. An intron, also called an intervening sequence, is defined in the art as a part of a primary transcript, or DNA encoding it, that is removed by splicing during RNA processing and is not included in the mature, functional mRNA, rRNA or tRNA (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999).

As disclosed in the specification, SEQ ID NOS: 24-28 are derived from the BS322 molecule. As shown in Jager *et al.*, *supra*, and in Applicants' disclosure, mRNA expressions of the gene, i.e., sequence segments from the genes which encode proteins that have a specific epitope, are useful as markers for breast diseases. Thus, for these reasons, Applicants respectfully request the Examiner to withdraw the rejection of claims 52-61, 70 and 77- 35 under 35 U.S.C. § 101 and § 112, first paragraph, and allow the claims.

## **CONCLUSION**

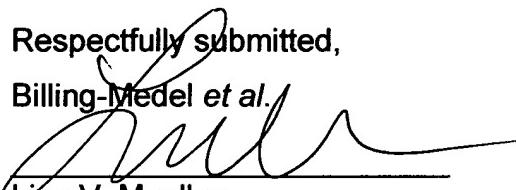
Applicants respectfully submit that the claims comply with the requirements of 35 U.S.C. Sections 101, 112, 102 and 103. Accordingly, a Notice of Allowance is believed in order and is respectfully requested.

Should the Examiner have any questions concerning the above, she is respectfully requested to contact the undersigned at the telephone number listed below. If the Examiner notes any further matters which the Examiner believes may be expedited by a telephone interview, the Examiner is requested to contact the undersigned.

If any additional fees are incurred as a result of the filing of this paper, authorization is given to charge deposit account no. 23-0785.

Respectfully submitted,

Billing-Medel et al.

  
Lisa V. Mueller  
Registration No. 38,978  
Attorney for Applicants

Wood, Phillips, Katz, Clark & Mortimer  
500 West Madison Street  
Suite 3800  
Chicago, IL 60662-2511

Tel.: (312) 876-2109  
Fax.: (312) 876-2020

BS322 Contig summary1.TXT  
Summary View of Contig "Contig[0013]"

>AF269087	#1	CTAGTCTATA CCAGCAACGA CTCCTACATC ..... CTAGTCTATA CCAGCAACGA CTCCTACATC
>AF269087	#31	GTCCACTCTG GGGATCTTAG AAAGATCCAT ..... GTCCACTCTG GGGATCTTAG AAAGATCCAT
>AF269087	#61	AAAGCTGCCT CCCGGGGACA AGTCCGGAAG ..... AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
>AF269087	#91	CTGGAGAAGA TGACAAAGAG GAAGAAGACC ..... CTGGAGAAGA TGACAAAGAG GAAGAAGACC
>AF269087	#121	ATCAACCTTA ATATACAAGA CGCCCAGAAC ..... ATCAACCTTA ATATACAAGA CGCCCAGAAC
>AF269087	#151	AGGACTGCTC TACACTGGGC CTGTGTCAAT ..... AGGACTGCTC TACACTGGGC CTGTGTCAAT
>AF269087	#181	GGCCATGAGG AAGTAGTAAC ATTTCTGGTA ..... GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
>AF269087	#211	GACAGAAAGT GCCAGCTTGA CGTCCTTGAT ..... GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
>AF269087	#241	GGCGAACACA GGACACCTCT GATGAAGGCT ..... GGCGAACACA GGACACCTCT GATGAAGGCT
>AF269087	#271	CTACAATGCC ATCAGGAGGC TTGTGCAAAT ..... CTACAATGCC ATCAGGAGGC TTGTGCAAAT
>AF269087	#301	ATTCTGATAG ATTCTGGTGC CGATATAAAT ..... ATTCTGATAG ATTCTGGTGC CGATATAAAT
>AF269087	#331	CTCGTAGATG TGTATGGCAA CATGGCTCTC ..... CTCGTAGATG TGTATGGCAA CATGGCTCTC

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>AF269087	#361	CATTATGCTG TTTATAGTGA GATTTTGTCA ..... CATTATGCTG TTTATAGTGA GATTTTGTCA
>AF269087	#391	GTGGTGGCAA AACTGCTGTC CCATGGTGCA ..... GTGGTGGCAA AACTGCTGTC CCATGGTGCA
>AF269087	#421	GTCATCGAAG TGCAACAACAA GGCTAGCCTC ..... GTCATCGAAG TGCAACAACAA GGCTAGCCTC
>AF269087	#451	ACACCACTTT TACTATCCAT AACGAAAAGA ..... ACACCACTTT TACTATCCAT AACGAAAAGA
>AF269087	#481	AGTGAGCAA TTGTGGAATT TTTGCTGATA ..... AGTGAGCAA TTGTGGAATT TTTGCTGATA
>AF269087	#511	AAAAATGCAA ATGCGAATGC AGTTAATAAG ..... AAAAATGCAA ATGCGAATGC AGTTAATAAG
>AF269087	#541	TATAAATGCA CAGCCCTCAT GCTTGCTGTA ..... TATAAATGCA CAGCCCTCAT GCTTGCTGTA
>AF269087	#571	TGTCATGGAT CATCAGAGAT AGTTGGCATG ..... TGTCATGGAT CATCAGAGAT AGTTGGCATG
>AF269087	#601	CTTCTTCAGC AAAATGTTGA CGTCTTGCT ..... CTTCTTCAGC AAAATGTTGA CGTCTTGCT
>AF269087	#631	GCAGATATAT GTGGAGTAAC TGCAGAACAT ..... GCAGATATAT GTGGAGTAAC TGCAGAACAT
>AF269087	#661	TATGCTGTTA CTTGTGGATT TCATCACATT ..... TATGCTGTTA CTTGTGGATT TCATCACATT
>AF269087	#691	CATGAACAAA TTATGGAATA TATACGAAAA ..... CATGAACAAA TTATGGAATA TATACGAAAA
>AF269087	#721	TTATCTAAAA ATCATCAAAA TACCAATCCA ..... TTATCTAAAA ATCATCAAAA TACCAATCCA

BS322 Contig summary1.TXT

>AF269087	#751	GAAGGAACAT CTGCAGGAAC ACCTGATGAG ..... GAAGGAACAT CTGCAGGAAC ACCTGATGAG
>AF269087	#781	GCTGCACCT TGGCGGAAAG AACACCTGAC ..... GCTGCACCT TGGCGGAAAG AACACCTGAC
>AF269087	#811	ACAGCTGAAA GCTTGGTGG AAAAAACACCT ..... ACAGCTGAAA GCTTGGTGG AAAAAACACCT
>AF269087	#841	GATGAGGCTG CACCCTTGGT GGAAAGAAC ..... GATGAGGCTG CACCCTTGGT GGAAAGAAC
>AF269087	#871	CCTGACACGG CTGAAAGCTT GGTGGAAAAA ..... CCTGACACGG CTGAAAGCTT GGTGGAAAAA
>AF269087	#901	ACACCTGATG AGGCTGCATC CTTGGTGGAG ..... ACACCTGATG AGGCTGCATC CTTGGTGGAG
>AF269087	#931	GGAACATCTG ACAAAATTCA ATGTTGGAG ..... GGAACATCTG ACAAAATTCA ATGTTGGAG
>AF269087	#961	AAAGCGACAT CTGGAAAGTT CGAACAGTCA ..... AAAGCGACAT CTGGAAAGTT CGAACAGTCA
>AF269087	#991	GCAGAAGAAA CACCTAGGGA AATTACGAGT ..... GCAGAAGAAA CACCTAGGGA AATTACGAGT
>AF269087	#1021	CCTGCAAAAG AAACATCTGA GAAATTACG ..... CCTGCAAAAG AAACATCTGA GAAATTACG
>AF269087	#1051	TGGCCAGCAA AAGGAAGACC TAGGAAGATC ..... TGGCCAGCAA AAGGAAGACC TAGGAAGATC
>AF269087	#1081	GCATGGGAGA AAAAAGAAGA CACACCTAGG ..... GCATGGGAGA AAAAAGAAGA CACACCTAGG
>AF269087	#1111	GAAATTATGA GTCCCGCAAA AGAAACATCT

BS322 Contig summary1.TXT

	#1111	GAAATTATGA GTCCCGCAAA AGAAACATCT
>AF269087	#1141	GAGAAATTAA CGTGGGCAGC AAAAGGAAGA
	#1141	GAGAAATTAA CGTGGGCAGC AAAAGGAAGA
>AF269087	#1171	CCTAGGAAGA TCGCATGGGA GAAAAAAAGAA
	#1171	CCTAGGAAGA TCGCATGGGA GAAAAAAAGAA
>AF269087	#1201	ACACCTGTAA AGACTGGATG CGTGGCAAGA
	#1201	ACACCTGTAA AGACTGGATG CGTGGCAAGA
>AF269087	#1231	GTAACATCTA ATAAAACCAA AGTTTTGGAA
	#1231	GTAACATCTA ATAAAACCAA AGTTTTGGAA
>AF269087	#1261	AAAGGAAGAT CTAAGATGAT TGCAATGTCCT
	#1261	AAAGGAAGAT CTAAGATGAT TGCAATGTCCT
>AF269087	#1291	ACAAAAGAACATCTACAAA AGCAAGTGCC
	#1291	ACAAAAGAACATCTACAAA AGCAAGTGCC
>AF269087	#1321	AATGATCAGA GGTTCCCATC AGAATCCAAA
	#1321	AATGATCAGA GGTTCCCATC AGAATCCAAA
>AF269087	#1351	CAAGAGGAAG ATGAAGAATA TTCTTGATGAT
	#1351	CAAGAGGAAG ATGAAGAATA TTCTTGATGAT
>AF269087	#1381	TCTCGGAGTC TCTTGAGAG TTCTGCAAAG
	#1381	TCTCGGAGTC TCTTGAGAG TTCTGCAAAG
>AF269087	#1411	ATTCAAGTGT GTATACCTGA GTCTATATAT
	#1411	ATTCAAGTGT GTATACCTGA GTCTATATAT
>AF269087	#1441	CAAAAAGTAA TGGAGATAAA TAGAGAAGTA
	#1441	CAAAAAGTAA TGGAGATAAA TAGAGAAGTA
>AF269087	#1471	GAAGAGCCTC CTAAGAAGCC ATCTGCCTTC
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BS322 Contig summary1.TXT

>AF269087	#1501	AAGCCTGCCA TTGAAATGCA AAACTCTGTT .....
	#1501	AAGCCTGCCA TTGAAATGCA AAACTCTGTT .....
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	#1531	CCAAATAAAG CCTTGATT GAAGAATGAA .....
>AF269087	#1561	CAAACATTGA GAGCAGATCC GATGTTCCA .....
	#1561	CAAACATTGA GAGCAGATCC GATGTTCCA .....
>AF269087	#1591	CCAGAATCCA AACAAAAGGA CTATGAAGAA .....
	#1591	CCAGAATCCA AACAAAAGGA CTATGAAGAA .....
>AF269087	#1621	AATTCTTGGG ATTCTGAGAG TCTCTGTGAG .....
	#1621	AATTCTTGGG ATTCTGAGAG TCTCTGTGAG .....
>AF269087	#1651	ACTGTTCAC AGAAGGATGT GTGTTACCC .....
	#1651	ACTGTTCAC AGAAGGATGT GTGTTACCC .....
>AF269087	#1681	AAGGCTACAC ATCAAAAAGA AATAGATAAA .....
	#1681	AAGGCTACAC ATCAAAAAGA AATAGATAAA .....
>AF269087	#1711	ATAAATGGAA ATTAGAAGA GTCTCCTAAT .....
	#1711	ATAAATGGAA ATTAGAAGA GTCTCCTAAT .....
>AF269087	#1741	AAAGATGGTC TTCTGAAGGC TACCTGCGGA .....
	#1741	AAAGATGGTC TTCTGAAGGC TACCTGCGGA .....
>AF269087	#1771	ATGAAAGTTT CTATTCCAAC TAAAGCCTTA .....
	#1771	ATGAAAGTTT CTATTCCAAC TAAAGCCTTA .....
>AF269087 >BS322 1 to 1198	#1801 >#1>  #1801	GAATTGAAGG ACATGCAAAC TTTCAAAGCG AGTATAC ATTCTTTATT ..... GAATTGAAGG ACAGWYAWAC WTTCTWWRYK * * * * * *****
>AF269087 >BS322 1 to 1198	#1831 #18  #1831	GAGCCTCCGG GGAAGCCATC TGCCCTCGAG AATCAT:TT TGCTTCCAAC :CCCATTAG ..... RAKCMTCCKK KGMWKCCAWC TSCCWTYKAG * * * **** * *** * * * * *

		BS322 Contig summary1.TXT
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>AF269087 >BS322 1 to 1198	#1891 #78  #1891	AATAAAGCCT TGGAATTGAA AAATGAACAA AATAAAGCCT TGGAATTGAA GAATGAACAA AATAAAGCCT TGGAATTGAA RAATGAACAA * .....
>AF269087 >BS322 1 to 1198	#1921 #108  #1921	ACATGGAGAG CAGATGAGAT ACTCCCATCA ACATTGAGAG CAGATGAGAT ACTCCCATCA ACATKGAGAG CAGATGAGAT ACTCCCATCA * .....
>AF269087 >BS322 1 to 1198	#1951 #138  #1951	GAATCCAAAC AAAAGGACTA TGAAGAAAAT GAATCCAAAC AAAAGGACTA TGAAGAAAGT GAATCCAAAC AAAAGGACTA TGAAGAAART * .....
>AF269087 >BS322 1 to 1198	#1981 #168  #1981	TCTTGGGATA CTGAGAGTCT CTGTGAGACT TCTTGGGATT CTGAGAGTCT CTGTGAGACT TCTTGGGATW CTGAGAGTCT CTGTGAGACT * .....
>AF269087 >BS322 1 to 1198	#2011 #198  #2011	GTTTCACAGA AGGATGTGTG TTTACCCAAG GTTTCACAGA AGGATGTGTG TTTACCCAAG GTTTCACAGA AGGATGTGTG TTTACCCAAG .....
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>AF269087 >BS322 1 to 1198	#2071 #258  #2071	AATGGAAAAT TAGAAGGGTC TCCTGTTAAA AATGGAAAAT TAGAAGGGTC TCCTGTTAAA AATGGAAAAT TAGAAGGGTC TCCTGTTAAA .....
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>AF269087 >BS322 1 to 1198	#2161 #348	TTGATGGACA TGCAAACHTT CAAAGCAGAG TTGATGGACA TGCAAACHTT CAAAGCAGAG .....

BS322 Contig summary1.TXT		
	#2161	TTGATGGACA TGCAAACCTT CAAAGCAGAG
>AF269087 >BS322 1 to 1198	#2191 #378  #2191	CCTCCCGAGA AGCCATCTGC CTTCGAGCCT CCTCCCGAGA AGCCATCTGC CTTCGAGCCT CCTCCCGAGA AGCCATCTGC CTTCGAGCCT
>AF269087 >BS322 1 to 1198	#2221 #408  #2221	GCCATTGAAA TGCAAAAGTC TGTTCCAAT GCCATTGAAA TGCAAAAGTC TGTTCCAAT GCCATTGAAA TGCAAAAGTC TGTTCCAAT
>AF269087 >BS322 1 to 1198	#2251 #438  #2251	AAAGCCTTGG AATTGAAGAA TGAACAAACA AAAGCCTTGG AATTGAAGAA TGAACAAACA AAAGCCTTGG AATTGAAGAA TGAACAAACA
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>AF269087 >BS322 1 to 1198	#2371 #558  #2371	TCACAGAAGG ATGTGTGTTT ACCCAAGGCT TCACAGAAGG ATGTGTGTTT ACCCAAGGCT TCACAGAAGG ATGTGTGTTT ACCCAAGGCT
>AF269087 >BS322 1 to 1198	#2401 #588  #2401	ACACATCAAA AAGAAATAGA TAAAATAAAT ACACATCAAA AAGAAATAGA TAAAATAAAT ACACATCAAA AAGAAATAGA TAAAATAAAT
>AF269087 >BS322 1 to 1198	#2431 #618  #2431	GGAAAATTAG AAGAGTCTCC TGATAATGAT GGAAAATTAG AAGAGTCTCC TGATAATGAT GGAAAATTAG AAGAGTCTCC TGATAATGAT
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BS322 Contig summary1.TXT			
>AF269087	#2491	GT	TTCTATTCAACTAAAGCCTTAGAATTG
>BS322 1 to 1198	#678	GT	TTCTATTCAACTAAAGCCTTAGAATTG
	#2491	GT	TTCTATTCAACTAAAGCCTTAGAATTG
>AF269087	#2521	ATGGACATGC	AAACTTCAAAGCAGAGCCT
>BS322 1 to 1198	#708	ATGGACATGC	AAACTTCAAAGCAGAGCCT
	#2521	ATGGACATGC	AAACTTCAAAGCAGAGCCT
>AF269087	#2551	CCCGAGAAC	CATCTGCCTT CGAGCCTGCC
>BS322 1 to 1198	#738	CCCGAGAAC	CATCTGCCTT CGAGCCTGCC
	#2551	CCCGAGAAC	CATCTGCCTT CGAGCCTGCC
>AF269087	#2581	ATTGAAATGC	AAAAGTCTGT TCCAAATAAA
>BS322 1 to 1198	#768	ATTGAAATGC	AAAAGTCTGT TCCAAATAAA
	#2581	ATTGAAATGC	AAAAGTCTGT TCCAAATAAA
>AF269087	#2611	GCCTTGAAT	TGAAGAATGA ACAAACATTG
>BS322 1 to 1198	#798	GCCTTGAAT	TGAAGAATGA ACAAACATTG
	#2611	GCCTTGAAT	TGAAGAATGA ACAAACATTG
>AF269087	#2641	AGAGCAGATC	AGATGTTCCC TTCAGAACATCA
>BS322 1 to 1198	#828	AGAGCAGATC	AGATGTTCCC TTCAGAACATCA
	#2641	AGAGCAGATC	AGATGTTCCC TTCAGAACATCA
>AF269087	#2671	AAACAAAAGA	AGTTGAAGA AAATTCTTGG
>BS322 1 to 1198	#858	AAACAAAAGA	ACGTTGAAGA AAATTCTTGG
	#2671	AAACAAAAGA	ASGTTGAAGA AAATTCTTGG
*			
>AF269087	#2701	GATTCTGAGA	GTCTCCGTGA GACTGTTCA
>BS322 1 to 1198	#888	GATTCTGAGA	GTCTCCGTGA GACTGTTCA
	#2701	GATTCTGAGA	GTCTCCGTGA GACTGTTCA
>AF269087	#2731	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
>BS322 1 to 1198	#918	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
	#2731	CAGAAGGATG	TGTGTGTACC CAAGGCTACA
>AF269087	#2761	CATCAAAAAG	AAATGGATAA AATAAGTGG
>BS322 1 to 1198	#948	CATCAAAAAG	AAATGGATAA AATAAGTGG
	#2761	CATCAAAAAG	AAATGGATAA AATAAGTGG
>AF269087	#2791	AAATTAGAAG	ATTCAACTAG CCTATCAAAA
>BS322 1 to 1198	#978	AAATTAGAAG	ATTCAACTAG CCTATCAAAA

		BS322 Contig summary1.TXT
	#2791	AAATTAGAAG ATTCAACTAG CCTATCAAAA
>AF269087 >BS322 1 to 1198	#2821 #1008  #2821	ATCTTGGATA CAGTCATTC TTGTGAAAGA ATCTTGGATA CAATTCATTC TTGTGAAAGA ATCTTGGATA CARTTCATTC TTGTGAAAGA *
>AF269087 >BS322 1 to 1198	#2851 #1038  #2851	GCAAGGGAAC TTCAAAAAGA TCACTGTGAA GCAAGGGAAC TTCAAAAAGA TCACTGTGAA GCAAGGGAAC TTCAAAAAGA TCACTGTGAA
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>AF269087 >BS322 1 to 1198	#2911 #1098  #2911	AAGAAGTTT GTGTACTGAA AAAGAAACTG AAGAAGTTT GTGTACTGAA AAAGAAACTG AAGAAGTTT GTGTACTGAA AAAGAAACTG
>AF269087 >BS322 1 to 1198	#2941 #1128  #2941	TCAGAAGCAA AAGAAATAAA ATCACAGTTA TCAGAAGCAA AAGAAATAAA ATCACAGTTA TCAGAAGCAA AAGAAATAAA ATCACAGTTA
>AF269087 >BS322 1 to 1198	#2971 #1158  #2971	GAGAACCAAA AAGTTAAATG GGAACAAGAG GAGAACCAAA AAGTTAAATG GGAACAAGAG GAGAACCAAA AAGTTAAATG GGAACAAGAG
>AF269087 >BS322 1 to 1198	#3001 #1188  #3001	CTCTGCAGTG TGAGATTGAC TTTAAACCAA CTCTGCAGTG TGAGATTGAC TTTAAACCAA CTCTGCAGTG TGAGATTGAC TTTAAACCAA
>AF269087	#3031  #3031	GAAGAAGAGA AGAGAAGAAA TGCCGATATA GAAGAAGAGA AGAGAAGAAA TGCCGATATA
>AF269087	#3061  #3061	TTAAATGAAA AAATTAGGGA AGAATTAGGA TTAAATGAAA AAATTAGGGA AGAATTAGGA
>AF269087	#3091  #3091	AGAATCGAAG AGCAGCATAG GAAAGAGTTA AGAATCGAAG AGCAGCATAG GAAAGAGTTA
>AF269087	#3121  #3121	GAAGTGAAAC AACAACTTGA ACAGGCTCTC GAAGTGAAAC AACAACTTGA ACAGGCTCTC

BS322 Contig summary1.TXT

>AF269087	#3151	AGAATACAAG ATATAGAATT GAAGAGTGTA ..... AGAATACAAG ATATAGAATT GAAGAGTGTA
>BS322 1199 to 2683 >#1> >AF269087	#3181	GT TTCTCACACT GAAAGTAATT TGAATCAGGT TTCTCACACT ..... GAAAGTAATT TGAATCAGGT TTCTCACACT
>BS322 1199 to 2683 #13 >AF269087	#3211	CATGAAAATG AAAATTATCT CTTACATGAA CATGAAAATG AAAATTATCT CTTACATGAA ..... CATGAAAATG AAAATTATCT CTTACATGAA
>BS322 1199 to 2683 #43 >AF269087	#3241	AATTGCATGT TGAAAAAGGA AATTGCCATG AATTGCATGT TGAAAAAGGA AATTGCCATG ..... AATTGCATGT TGAAAAAGGA AATTGCCATG
>BS322 1199 to 2683 #73 >AF269087	#3271	CTAAAACCTGG AAATAGCCAC ACTGAAACAC CTAAAACCTGG AAATAGCCAC ACTGAAACAC ..... CTAAAACCTGG AAATAGCCAC ACTGAAACAC
>BS322 1199 to 2683 #103 >AF269087	#3301	CAATACCAGG AAAAGGAAAA TAAATACTTT CAATACCAGG AAAAGGAAAA TAAATACTTT ..... CAATACCAGG AAAAGGAAAA TAAATACTTT
>BS322 1199 to 2683 #133 >AF269087	#3331	GAGGACATTA AGATTTAAA AGAAAAGAAT GAGGACATTA AGATTTAAA AGAAAAGAAT ..... GAGGACATTA AGATTTAAA AGAAAAGAAT
>BS322 1199 to 2683 #163 >AF269087	#3361	GCTGAACCTTC AGATGACCCCT AAAACTGAAA GCTGAACCTTC AGATGACCCCT AAAACTGAAA ..... GCTGAACCTTC AGATGACCCCT AAAACTGAAA
>BS322 1199 to 2683 #193 >AF269087	#3391	GAGGAATCAT TAACTAAAAG GGCATCTCAA GAGGAATCAT TAACTAAAAG GGCATCTCAA ..... GAGGAATCAT TAACTAAAAG GGCATCTCAA
>BS322 1199 to 2683 #223 >AF269087	#3421	TATAGTGGGC AGCTTAAAGT TCTGATAGCT TATAGTGGGC AGCTTAAAGT TCTGATAGCT ..... TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>BS322 1199 to 2683 #253 >AF269087	#3451	GAGAACACAA TGCTCACTTC TAAATTGAAG GAGAACACAA TGCTCACTTC TAAATTGAAG

BS322 Contig summary1.TXT

#3451	GAGAACACAA TGCTCACTTC TAAATTGAAG
>BS322 1199 to 2683 #283 >AF269087 #3481	GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA GAAAAACAAG ACAAAAGAAAT ACTAGAGGCA
#3481	
>BS322 1199 to 2683 #313 >AF269087 #3511	GAAATTGAAT CACACCATCC TAGACTGGCT GAAATTGAAT CACACCATCC TAGACTGGCT GAAATTGAAT CACACCATCC TAGACTGGCT
#3511	
>BS322 1199 to 2683 #343 >AF269087 #3541	TCTGCTGTAC AAGACCATGA TCAAATTGTG TCTGCTGTAC AAGACCATGA TCAAATTGTG TCTGCTGTAC AAGACCATGA TCAAATTGTG
#3541	
>BS322 1199 to 2683 #373 >AF269087 #3571	ACATCAAGAA AAAGTCAAGA ACCTGCTTTC ACATCAAGAA AAAGTCAAGA ACCTGCTTTC ACATCAAGAA AAAGTCAAGA ACCTGCTTTC
#3571	
>BS322 1199 to 2683 #403 >AF269087 #3601	CACATTGCAG GAGATGCTTG TTTGCAAAGA CACATTGCAG GAGATGCTTG TTTGCAAAGA CACATTGCAG GAGATGCTTG TTTGCAAAGA
#3601	
>BS322 1199 to 2683 #433 >AF269087 #3631	AAAATGAATG TTGATGTGAG TAGTACGATA AAAATGAATG TTGATGTGAG TAGTACGATA AAAATGAATG TTGATGTGAG TAGTACGATA
#3631	
>BS322 1199 to 2683 #463 >AF269087 #3661	TATAACAATG AGGTGCTCCA TCAACCACTT TATAACAATG AGGTGCTCCA TCAACCACTT TATAACAATG AGGTGCTCCA TCAACCACTT
#3661	
>BS322 1199 to 2683 #493 >AF269087 #3691	TCTGAAGCTC AAAGGAAATC CAAAAGCCTA TCTGAAGCTC AAAGGAAATC CAAAAGCCTA TCTGAAGCTC AAAGGAAATC CAAAAGCCTA
#3691	
>BS322 1199 to 2683 #523 >AF269087 #3721	AAAATTAATC TCAATTATGC AGGAGATGCT AAAATTAATC TCAATTATGC AGGAGATGCT AAAATTAATC TCAATTATGC AGGAGATGCT
#3721	
>BS322 1199 to 2683 #553 >AF269087 #3751	CTAAGAGAAA ATACATTGGT TTCAGAACAT CTAAGAGAAA ATACATTGGT TTCAGAACAT CTAAGAGAAA ATACATTGGT TTCAGAACAT
#3751	

BS322 Contig summary1.TXT

>BS322 1199 to 2683 #583		GCACAAAGAG ACCAACGTGA AACACAGTGT
>AF269087	#3781	GCACAAAGAG ACCAACGTGA AACACAGTGT
	#3781	..... GCACAAAGAG ACCAACGTGA AACACAGTGT
>BS322 1199 to 2683 #613		CAAATGAAGG AAGCTGAACA CATGTATCAA
>AF269087	#3811	CAAATGAAGG AAGCTGAACA CATGTATCAA
	#3811	..... CAAATGAAGG AAGCTGAACA CATGTATCAA
>BS322 1199 to 2683 #643		AACGAACAAG ATAATGTGAA CAAACACACT
>AF269087	#3841	AACGAACAAG ATAATGTGAA CAAACACACT
	#3841	..... AACGAACAAG ATAATGTGAA CAAACACACT
>BS322 1199 to 2683 #673		GAACAGCAGG AGTCTCTAGA TCAGAAATTAA
>AF269087	#3871	GAACAGCAGG AGTCTCTAGA TCAGAAATTAA
	#3871	..... GAACAGCAGG AGTCTCTAGA TCAGAAATTAA
>BS322 1199 to 2683 #703		TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>AF269087	#3901	TTTCAACTAC AAAGCAAAAA TATGTGGCTT
	#3901	..... TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>BS322 1199 to 2683 #733		CAACAGCAAT TAGTCATGC ACATAAGAAA
>AF269087	#3931	CAACAGCAAT TAGTCATGC ACATAAGAAA
	#3931	..... CAACAGCAAT TAGTCATGC ACATAAGAAA
>BS322 1199 to 2683 #763		GCTGACAACA AAAGCAAGAT ACAATTGAT
>AF269087	#3961	GCTGACAACA AAAGCAAGAT ACAATTGAT
	#3961	..... GCTGACAACA AAAGCAAGAT ACAATTGAT
>BS322 1199 to 2683 #793		ATTCATTTTC TTGAGAGGAA AATGCAACAT
>AF269087	#3991	ATTCATTTTC TTGAGAGGAA AATGCAACAT
	#3991	..... ATTCATTTTC TTGAGAGGAA AATGCAACAT
>BS322 1199 to 2683 #823		CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>AF269087	#4021	CATCTCCTAA AAGAGAAAAA TGAGGAGATA
	#4021	..... CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>BS322 1199 to 2683 #853		TTTAATTACA ATAACCATT AAAAACCGT
>AF269087	#4051	TTTAATTACA ATAACCATT AAAAACCGT
	#4051	..... TTTAATTACA ATAACCATT AAAAACCGT
>BS322 1199 to 2683 #883		ATATATCAAT ATGAAAAAGA GAAAGCAGAA
>AF269087	#4081	ATATATCAAT ATGAAAAAGA GAAAGCAGAA

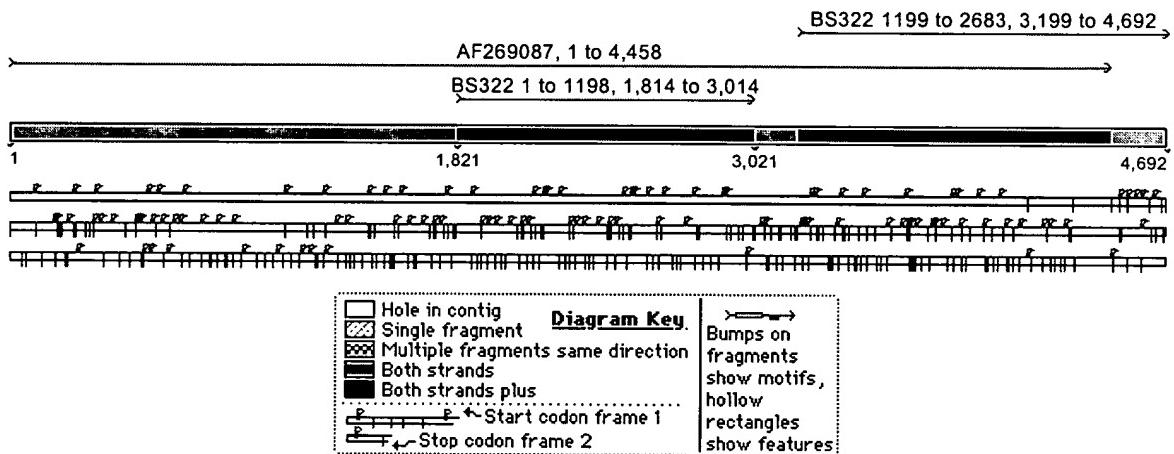
BS322 Contig summary1.TXT

#4081	..... ATATATCAAT ATGAAAAAGA GAAAGCAGAA
>BS322 1199 to 2683 #913 >AF269087	ACAGAAAACT CATGAGAGAC AAGCAGTAAG ACAGAAAACT CATGAGAGAC AAGCAGTAAG ..... ACAGAAAACT CATGAGAGAC AAGCAGTAAG
#4111	
#4111	
>BS322 1199 to 2683 #943 >AF269087	AAACTTCTTT TGGAGAAACA ACAGACCAGA AAACTTCTTT TGGAGAAACA ACAGACCAGA ..... AAACTTCTTT TGGAGAAACA ACAGACCAGA
#4141	
#4141	
>BS322 1199 to 2683 #973 >AF269087	TCTTTACTCA CAACTCATGC TAGGAGGCCA TCTTTACTCA CAACTCATGC TAGGAGGCCA ..... TCTTTACTCA CAACTCATGC TAGGAGGCCA
#4171	
#4171	
>BS322 1199 to 2683 #1003 >AF269087	GTCCTAGCAT CACCTTATGT TGAAAATCTT GTCCTAGCAT CACCTTATGT TGAAAATCTT ..... GTCCTAGCAT CACCTTATGT TGAAAATCTT
#4201	
#4201	
>BS322 1199 to 2683 #1033 >AF269087	ACCAATAGTC TGTGTCAACA GAATACTTAT ACCAATAGTC TGTGTCAACA GAATACTTAT ..... ACCAATAGTC TGTGTCAACA GAATACTTAT
#4231	
#4231	
>BS322 1199 to 2683 #1063 >AF269087	TTTAGAAGAA AAATTCTATGA TTTCTTCCTG TTTAGAAGAA AAATTCTATGA TTTCTTCCTG ..... TTTAGAAGAA AAATTCTATGA TTTCTTCCTG
#4261	
#4261	
>BS322 1199 to 2683 #1093 >AF269087	AAGCCTACAG ACATAAAATA ACAGTGTGAA AAGCCTACAG ACATAAAATA ACAGTGTGAA ..... AAGCCTACAG ACATAAAATA ACAGTGTGAA
#4291	
#4291	
>BS322 1199 to 2683 #1123 >AF269087	GAATTACTTG TTCACGAA:T :C:TCGCTCT GAATTACTTG TTCACGAAATT GCATAAAGCT ..... GAATTACTTG TTCACGAAATT GCATMRMKCT * * * ***
#4321	
#4321	
>BS322 1199 to 2683 #1153 >AF269087	GCACCTCCA:G CCTAGGGGCC TAGTGAAACC GCACAGGATT CCCATCTACC CTGATGATGC ..... GCACWSSATK CCYAKSYRCC YWGWKRAWSC *** ** * *** ** *** *** **
#4351	
#4351	
>BS322 1199 to 2683 #1183 >AF269087	CTGTGTCA:A AAAGAAAA:A AACAAAAACA AGCAGACATC ATTCAATCCA ACCAGAACCT ..... MKSWGWCATM AWWSAAWMCA AMCARAACW **** * ** *** *** * * * *
#4381	
#4381	

BS322 Contig summary1.TXT

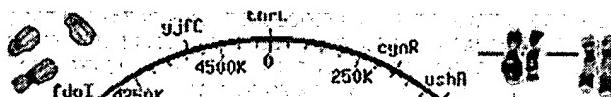
>BS322 1199 to 2683 #1213 >AF269087	#4411	AACCTCCAA GAC:CTCGA: GTGGTTTTG CGCTCTGCAC TCCAGCCTAG GTGACAGAGT ..... MRCTCTSCAM KMCASYCKAG GTGRYWKWKK ** * * * *** *** * * *****
>BS322 1199 to 2683 #1243 >AF269087	#4441	GAGACCCTGT ATCACTTCAA ATAATGTGTT GAGACTCCAC CTCGGAAA ..... GAGACYCYRY MTCRSWWMAA ATAATGTGTT * *** * *****
>BS322 1199 to 2683 #1273	#4471	AAACAAGCAT CTTCATCTCA TTAAATAGAA ..... AAACAAGCAT CTTCATCTCA TTAAATAGAA
>BS322 1199 to 2683 #1303	#4501	ATGTTGAAAA ATTGCTTTG GAATAATTGA ..... ATGTTGAAAA ATTGCTTTG GAATAATTGA
>BS322 1199 to 2683 #1333	#4531	CTTATGGATA TTTCATCAAA TTTACAGTTG ..... CTTATGGATA TTTCATCAAA TTTACAGTTG
>BS322 1199 to 2683 #1363	#4561	GCTATGCTTT CTTATTGTGC ATACTATGAA ..... GCTATGCTTT CTTATTGTGC ATACTATGAA
>BS322 1199 to 2683 #1393	#4591	ATGTTTTCT TCAAAAAGTG TTTATAAGTG ..... ATGTTTTCT TCAAAAAGTG TTTATAAGTG
>BS322 1199 to 2683 #1423	#4621	GTAAGTTAA GAATGGGGTT GACAGCATT ..... GTAAGTTAA GAATGGGGTT GACAGCATT
>BS322 1199 to 2683 #1453	#4651	TCTTTTGTTG TGATTTGATT AAACATTAC ..... TCTTTTGTTG TGATTTGATT AAACATTAC
>BS322 1199 to 2683 #1483	#4681	TAATTGTGCA TA .....

1. BS 322 contains 2683 nucleotides. This sequence was obtained by sequencing Incyte clone 4304443 in house.
  2. NY-BR-1 (AF269087) contains 4466 nucleotides.
  3. The contig (**below**) shows that BS322 is missing a single stretch of 185 nucleotides that are present in NY-BR-1. These nucleotides are missing between position 1198 and 1199 of BS322. The missing piece is nucleotides 3015 thru 3198 of NY-BR-1(AF269087). The first 45 bases of BS322 are a poor match to AF269087). The remaining bases are almost 100% identical. See BS322 contig summary file.
  4. It appears that Incyte clone 4304443 is a splice variant of NY-BR-1. The gap occurs in the open reading frame region.
  5. The primers used for the NY-BR-1 study were: Forward 2181 to 2202 and Reverse 3088 to 3111(AF269087). These primers are contained within BS322.





# results of BLAST



Entrez  
Genome

BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig  
545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

Show positions of the BLAST hits in the human genome using the Entrez  
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast  
cancer antigen NY-BR-1 mRNA, complete cds.  
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores

<40      40-50      50-80      80-200      >200

1\_2991

0 500 1000 1500 2000 2500 3000 3500 4000



Sequences producing significant alignments:

Score  
(bits)      E  
Value

ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genome...	1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genome...	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genome...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genome...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genome...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genome...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genome...	127	5e-26

Alignments

>ref|NT\_008705.14|Hs10\_8862 Homo sapiens chromosome 10 genomic contig  
Length = 20794168

Score = 1769 bits (920), Expect = 0.0  
Identities = 920/920 (100%)  
Strand = Plus / Plus

Query: 3197 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttggaaaa 3256  
Sbjct: 19483239 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttggaaaa 19483298

Query: 3257 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataccaggaaaagg 3316  
Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataccaggaaaagg 19483358

Query: 3317 aaaataaaatactttgaggacattaagatttaaaagaaaagaatgctgaacttcagatga 3376  
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Query: 3377 ccctaaaactgaaagaggaatcattaactaaaagggcatctcaatatagtggcagctta 3436  
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Query: 3437 aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaag 3496  
Sbjct: 19483479 aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaag 19483538

Query: 3497 aaatacttagaggcagaaattgaatcacaccatcctagactggcttcgtgtacaagacc 3556  
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Query: 3557 atgatcaaattgtgacatcaagaaaaagtcaagaacctgcttcacattgcaggagatg 3616  
Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgcttcacattgcaggagatg 19483658

Query: 3617 ctgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatatataacaatgaggc 3676  
Sbjct: 19483659 ctgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatatataacaatgaggc 19483718

Query: 3677 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaattatctcaatt 3736  
Sbjct: 19483719 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaattatctcaatt 19483778

Query: 3737 atgcaggagatgctctaagagaaaaatcatggttcagaacatgcacaaagagaccaac 3796  
Sbjct: 19483779 atgcaggagatgctctaagagaaaaatcatggttcagaacatgcacaaagagaccaac 19483838

Query: 3797 gtgaaacacagtgtcaaattgaagggaaatcatggttcagaacatgttatcaaaacgaacaagataatg 3856  
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Query: 3857 tgaacaaacacactgaacacgcaggagtctctagatcagaattttcaactacaagca 3916  
Sbjct: 19483899 tgaacaaacacactgaacacgcaggagtctctagatcagaattttcaactacaagca 19483958

Query: 3917 aaaatatgtggcttcaacagcaatttagttcatgcacataagaaagctgacaacaaaagca 3976  
Sbjct: 19483959 aaaatatgtggcttcaacagcaatttagttcatgcacataagaaagctgacaacaaaagca 19484018

Query: 3977 agataacaattgatattcatttctttagagggaaaatgcaacatcatctcctaaaagaga 4036  
| |||||||  
Sbjct: 19484019 agataacaattgatattcatttctttagagggaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 4096  
| |||||||  
Sbjct: 19484079 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116  
| |||||||  
Sbjct: 19484139 aagagaaagcagaaacagaa 19484158

Score = 1108 bits (576), Expect = 0.0  
Identities = 576/576 (100%)  
Strand = Plus / Plus

Query: 749 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcgaaagaacacctg 808  
| |||||||  
Sbjct: 19405975 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcgaaagaacacctg 19406034

Query: 809 acacagctgaaagcttggggaaaaaacacctgatgaggctgcacccttgggaaagaa 868  
| |||||||  
Sbjct: 19406035 acacagctgaaagcttggggaaaaaacacctgatgaggctgcacccttgggaaagaa 19406094

Query: 869 cacctgacacggctgaaagcttggggaaaaaacacctgatgaggctgcaccccttggg 928  
| |||||||  
Sbjct: 19406095 cacctgacacggctgaaagcttggggaaaaaacacctgatgaggctgcaccccttggg 19406154

Query: 929 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTCTGAACAGT 988  
| |||||||  
Sbjct: 19406155 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTCTGAACAGT 19406214

Query: 989 cagcagaagaaacaccttagggaaattacgagtccctgcaaaagaaacatctgagaaattta 1048  
| |||||||  
Sbjct: 19406215 cagcagaagaaacaccttagggaaattacgagtccctgcaaaagaaacatctgagaaattta 19406274

Query: 1049 cgtggccagcaaaaggaagacaccttaggaagatcgcatggggagaaaaagaagacacaccta 1108  
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Sbjct: 19406335 gggAAATTATGAGTCCCGCAAAAGAAACACATCTGAGAAATTACGTGGGAGCAGCAAAAGGAA 19406394

Query: 1169 gaccttaggaagatcgcatggggagaaaaagaaaacacctgtaaagactggatgcgtggcaa 1228  
| |||||||  
Sbjct: 19406395 gaccttaggaagatcgcatggggagaaaaagaaaacacctgtaaagactggatgcgtggcaa 19406454

Query: 1229 gagtaacatctaataaaactaaagtttggaaaaaggaagatctaagatgattgcatgtc 1288  
| |||||||  
Sbjct: 19406455 gagtaacatctaataaaactaaagtttggaaaaaggaagatctaagatgattgcatgtc 19406514

Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324  
| |||||||

Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccatg 19406550

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Identities = 220/220 (100%)  
Strand = Plus / Plus

Query: 4117 aactcatgagagacaaggcgtaaagaaaacttctttggagaaacaacagaccagatcttta 4176  
|||||||  
Sbjct: 19495722 aactcatgagagacaaggcgtaaagaaaacttctttggagaaacaacagaccagatcttta 19495781

Query: 4177 ctcacaactcatgttaggaggccagtcctagcatcaccttatgttggaaaatcttaccaat 4236  
||| ||| ||| ||| |||  
Sbjct: 19495782 ctcacaactcatgttaggaggccagtcctagcatcaccttatgttggaaaatcttaccaat 19495841

Query: 4237 agtctgtcaacagaatacttatttagaaaaattcatgattcttcgtaaagcct 4296  
|||||  
Sbjct: 19495842 agtctgtcaacagaatacttatttagaaaaattcatgattcttcgtaaagcct 19495901

Query: 4297 acagacataaaaataacagtgtgaagaattacttgttacg 4336  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 19495902 acaqacataaaaataacaqtgtqaqaattacttgttacg 19495941

Score = 415 bits (216), Expect = e-113  
Identities = 219/220 (99%), Gaps = 1/220 (0%)  
Strand = Plus / Plus

Query: 2796 aga-agattcaactagcctatcaaaaatcttgatacagttcatttctgtgaaaggagcaa 2854  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 19480436 agacagattcaactagcctatcaaaaatcttgatacagttcatttctgtgaaaggagcaa 19480495

Query: 2855 gggacttcaaaaagatcactgtgaacaacgtacaggaaaaatgaaacaaatgaaaaaga 2914  
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Query: 2915 agttttgtgtactaaaaaaaactgtcagaagcaaaagaaataaaatcacagtttagaga 2974  
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Query: 3193            aatcaqqt 3200

Sbjct: 19482134 aatcaggt 19482141



# results of BLAST



BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig  
545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

Show positions of the BLAST hits in the human genome using the Entrez  
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast  
cancer antigen NY-BR-1 mRNA, complete cds.  
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

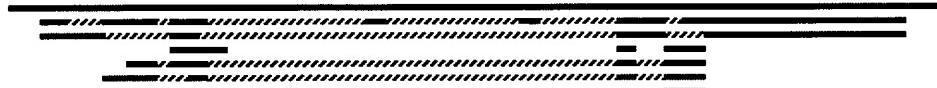
Mouse-over to show define and scores. Click to show alignments

Color Key for Alignment Scores

<40      40-50      50-80      80-200      >200

1\_2991

0 500 1000 1500 2000 2500 3000 3500 4000



Sequences producing significant alignments:

Score      E  
(bits)      Value

ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genomic DNA clone	1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genomic DNA clone	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genomic DNA clone	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genomic DNA clone	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic DNA clone	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genomic DNA clone	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic DNA clone	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic DNA clone	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genomic DNA clone	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genomic DNA clone	127	5e-26

Alignments

>ref|NT\_008705.14|Hs10\_8862 Homo sapiens chromosome 10 genomic contig  
Length = 20794168

Score = 1769 bits (920), Expect = 0.0  
Identities = 920/920 (100%)  
Strand = Plus / Plus

Query: 3197 aggttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttggaaaa 3256  
Sbjct: 19483239 aggttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttggaaaa 19483298

Query: 3257 aggaaattgccatgctaaaactggaaatagccacactgaaacccaataccaggaaaagg 3316  
Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacccaataccaggaaaagg 19483358

Query: 3317 aaaataaatactttgaggacattaagatTTaaaagaaaagaatgctgaacttcagatga 3376  
Sbjct: 19483359 aaaataaatactttgaggacattaagatTTaaaagaaaagaatgctgaacttcagatga 19483418

Query: 3377 ccctaaaactgaaagaggaatcattaactaaaaggcatctcaatatagtggcagctta 3436  
Sbjct: 19483419 ccctaaaactgaaagaggaatcattaactaaaaggcatctcaatatagtggcagctta 19483478

Query: 3437 aagttctgatagctgagaacacaatgctcaatttcaatttgaaggaaaaacaagacaag 3496  
Sbjct: 19483479 aagttctgatagctgagaacacaatgctcaatttcaatttgaaggaaaaacaagacaag 19483538

Query: 3497 aaatacttagaggcagaaattgaatcacaccatcctagactggcttgcgttacaagacc 3556  
Sbjct: 19483539 aaatacttagaggcagaaattgaatcacaccatcctagactggcttgcgttacaagacc 19483598

Query: 3557 atgatcaaattgtgacatcaagaaaaagtcaagaacctgcttccacattgcaggagatg 3616  
Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgcttccacattgcaggagatg 19483658

Query: 3617 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatatataacaatgaggc 3676  
Sbjct: 19483659 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatatataacaatgaggc 19483718

Query: 3677 tccatcaaccactttctgaagctcaaaggaaatccaaaaggctaaaaattatctcaatt 3736  
Sbjct: 19483719 tccatcaaccactttctgaagctcaaaggaaatccaaaaggctaaaaattatctcaatt 19483778

Query: 3737 atgcaggagatgctctaagagaaaatacattggttcagaacatgcacaaagagaccaac 3796  
Sbjct: 19483779 atgcaggagatgctctaagagaaaatacattggttcagaacatgcacaaagagaccaac 19483838

Query: 3797 gtgaaacacagtgtcaaattgaaggaagctgaacacatgttatcaaaacgaacaagataatg 3856  
Sbjct: 19483839 gtgaaacacagtgtcaaattgaaggaagctgaacacatgttatcaaaacgaacaagataatg 19483898

Query: 3857 tgaacaaacacactgaacacgcaggagttcttagatcagaattttcaactacaagca 3916  
Sbjct: 19483899 tgaacaaacacactgaacacgcaggagttcttagatcagaattttcaactacaagca 19483958

Query: 3917 aaaatatgtggcttcaacagcaattttcatgcacataagaaagctgacaacaaaagca 3976  
Sbjct: 19483959 aaaatatgtggcttcaacagcaattttcatgcacataagaaagctgacaacaaaagca 19484018

Query: 3977 agataacaattgatattcatttcttgagaggaaaatgcaacatcatctcctaaaagaga 4036  
| |||||||  
Sbjct: 19484019 agataacaattgatattcatttcttgagaggaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 4096  
| |||||||  
Sbjct: 19484079 aaaatgaggagatattaattacaataaccattaaaaaccgtatatcaatatgaaa 19484138

Query: 4097 aagagaaaagcagaaacagaa 4116  
| |||||||  
Sbjct: 19484139 aagagaaaagcagaaacagaa 19484158

Score = 1108 bits (576), Expect = 0.0  
Identities = 576/576 (100%)  
Strand = Plus / Plus

Query: 749 cagaaggaacatctgcaggAACACCTGATGAGGCTGCACCCCTGGCGGAAAGAACACCTG 808  
| |||||||  
Sbjct: 19405975 cagaaggaacatctgcaggAACACCTGATGAGGCTGCACCCCTGGCGGAAAGAACACCTG 19406034

Query: 809 acacagctgaaAGCTTGGTGGAAAAAACACCTGATGAGGCTGCACCCCTGGTGGAAAGAA 868  
| |||||||  
Sbjct: 19406035 acacagctgaaAGCTTGGTGGAAAAAACACCTGATGAGGCTGCACCCCTGGTGGAAAGAA 19406094

Query: 869 cacctgacacggctgaaAGCTTGGTGGAAAAAACACCTGATGAGGCTGCATCCTGGTGG 928  
| |||||||  
Sbjct: 19406095 cacctgacacggctgaaAGCTTGGTGGAAAAAACACCTGATGAGGCTGCATCCTGGTGG 19406154

Query: 929 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTTGAAACAGT 988  
| |||||||  
Sbjct: 19406155 agggAACATCTGACAAAATTCAATGTTGGAGAAAGCGACATCTGGAAAGTTGAAACAGT 19406214

Query: 989 cagcagaAGAAACACCTAGGGAAATTACGAGTCCTGCAAAAGAACATCTGGAAATTAA 1048  
| |||||||  
Sbjct: 19406215 cagcagaAGAAACACCTAGGGAAATTACGAGTCCTGCAAAAGAACATCTGGAAATTAA 19406274

Query: 1049 cgtggccagcaAAAGGAAGACCTAGGAAGATCGCATGGAGAAAAAGAAGACACACCTA 1108  
| |||||||  
Sbjct: 19406275 cgtggccagcaAAAGGAAGACCTAGGAAGATCGCATGGAGAAAAAGAAGACACACCTA 19406334

Query: 1109 gggAAATTATGAGTCCCAGAAAGAACATCTGGAAATTACGTGGGAGCAAAAGGAA 1168  
| |||||||  
Sbjct: 19406335 gggAAATTATGAGTCCCAGAAAGAACATCTGGAAATTACGTGGGAGCAAAAGGAA 19406394

Query: 1169 gaccttaggaAGATCGCATGGAGAAAAAGAACACCTGTAAGACTGGATGCGTGGCAA 1228  
| |||||||  
Sbjct: 19406395 gaccttaggaAGATCGCATGGAGAAAAAGAACACCTGTAAGACTGGATGCGTGGCAA 19406454

Query: 1229 gagtaACATCTAATAAAACTAAAGTTGGAAAAAGGAAGATCTAAGATGATTGATGTC 1288  
| |||||||  
Sbjct: 19406455 gagtaACATCTAATAAAACTAAAGTTGGAAAAAGGAAGATCTAAGATGATTGATGTC 19406514

Query: 1289 ctacaaaAGAACATCTACAAAAGCAAGTGCCAATG 1324  
| |||||||

Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccatg 19406550

Score = 423 bits (220), Expect = e-115  
Identities = 220/220 (100%)  
Strand = Plus / Plus

Query: 4117 aactcatgagagacaaggcgtaaacttctttggagaaacaacagaccagatctta 4176  
|||  
Sbjct: 19495722 aactcatgagagacaaggcgtaaacttctttggagaaacaacagaccagatctta 19495781

Query: 4177 ctcacaactcatgttagggccagtcctagcatcaccttatgttggaaatcttaccaat 4236  
|||  
Sbjct: 19495782 ctcacaactcatgttagggccagtcctagcatcaccttatgttggaaatcttaccaat 19495841

Query: 4297 acagacataaaaataacagtgtgaagaattacttgttacg 4336  
||||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 19495902 acaqacataaaaataacaqtgtqaqaattacttgttacg 19495941

Score = 415 bits (216), Expect = e-113  
Identities = 219/220 (99%), Gaps = 1/220 (0%)  
Strand = Plus / Plus

Query: 2796 aga-agattcaactagcctatcaaaaatcttgatcacagttcattttgtgaaagagcaa 2854  
||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 19480436 agacagattcaactagcctatcaaaaatcttgatcacagttcattttgtgaaagagcaa 19480495

Query: 2855 gggacttcaaaaagatcactgtacaacgtacaggaaaaatggaaatgaaaaaga 2914  
||| ||| ||| ||| ||| ||| |||  
Sbjct: 19480496 gggacttcaaaaagatcactgtacaacgtacaggaaaaatggaaatgaaaaaga 19480555

Query: 2915 agttttgtgtactgaaaaaaaactgtcagaagcaaaaagaaataaaatcacagtttagaga 2974  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Sbjct: 19480556 agttttgtgtactqaaaaaaaactgtcagaacqaaaaataaaatcacagttqaqqa 19480615

Query: 2975 accaaaaaggtaaatggaaacaagagctctgcagtgttag 3014  
|||||||  
Sbjct: 19480616 accaaaaaggtaaatqqqaaacaqaqcctctqcaqtqtqaq 19480655

Score = 362 bits (188), Expect = 1e-96  
Identities = 188/188 (100%)  
Strand = Plus / Plus

Query: 3013 agattgactttaaccaagaagaagagaagaaaatgccatatattaaatgaaaaaa 3072  
|||||||  
Sbjct: 19481954 aqattgactttaaccaagaqaqaqaaqaaqaaqaaatqcqcataatattaaatgaaaaaa 19482013

Query: 3073 attagggaagaatttaggaagaatcgaagagcagcataggaaagagttagaagttaaaaacaa 3132

Sbjct: 19482014 attagggagaat taggaagaatcgaaggagcgttagaaagagttagaagtgaaacaa 19482073

Query: 3133 caacttgaacaggctctcagaatacagaatataggatgttagaaagttaattg 3192

Query: 3193 aatcaggt

Sheet: 10182124 Date: 09/07/2013